

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: January 28, 2006, 08:01:18 ; Search time 545 Seconds
(without alignments)
5188.245 Million cell updates/sec

Title: US-10-664-234-18

Perfect score: 3404

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2632.6	77.3	4346	US-10-161-408-26	Sequence 26, Appl
5	2632.6	77.3	4479	US-11-149-403-30	Sequence 30, Appl
6	2632.6	77.3	5010	US-11-149-403-31	Sequence 31, Appl
7	2628.6	77.2	5414	US-11-149-403-32	Sequence 32, Appl
8	2625.8	77.1	5234	US-11-069-856-4	Sequence 4, Appl
9	2625.8	77.1	5775	US-11-069-856-12	Sequence 12, Appl
10	2625.8	77.1	5805	US-11-069-856-13	Sequence 13, Appl
11	2625.8	77.1	5909	US-11-069-856-15	Sequence 15, Appl
12	2625.8	77.1	6484	US-11-069-856-18	Sequence 18, Appl
13	2625.8	77.1	6514	US-11-069-856-21	Sequence 21, Appl
14	2621.6	77.0	2861	US-11-069-370-3	Sequence 3, Appl
15	2621.6	77.0	2861	US-11-069-631A-3	Sequence 3, Appl
16	2621.6	77.0	9632	US-10-893-584-1	Sequence 1, Appl
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18	2410	70.8	8970	US-10-641-678-31	Sequence 5, Appl
19	2410	70.8	10990	US-11-136-244-5	Sequence 17, Appl
20	2400	70.5	5988	US-11-159-919-17	Sequence 243, App
21	2391.6	70.3	3819	US-11-009-840A-243	Sequence 243, App
22	2391.6	70.3	3819	US-11-009-873A-243	Sequence 243, App

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ALIGNMENTS

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; Publication No. US20050255501A1
; GENERAL INFORMATION:
; APPLICANT: Ng, Patrick
; APPLICANT: Wei, Chialin
; APPLICANT: Ruan, Yifun
; TITLE OF INVENTION: Method for Gene Identification Signature (GIS) Analysis
; FILE REFERENCE: 3240-107
; CURRENT APPLICATION NUMBER: US/11/045,468A
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: 10/664,234

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; PRIOR FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 29
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; OTHER INFORMATION: bacterial cloning vector
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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7	2639.2	77.5	7387	3	US-09-867-947-28 Sequence 28, Appl
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9	2636.4	77.5	12225	7	US-10-646-628-1 Sequence 1, Appli
10	2634.6	77.4	4201	3	US-09-792-568-7 Sequence 7, Appli
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22	2633.6	77.4	3858	6	US-10-014-099F-14 Sequence 14, Appl
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ALIGNMENTS

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; Publication No. US20050059022A1
; GENERAL INFORMATION:
; APPLICANT: Ruan, Yijun
; APPLICANT: Ng, Patrick
; APPLICANT: Wei, Chialin
; TITLE OF INVENTION: Gene identification signature (GIS) analysis
; FILE REFERENCE: FP2027
; CURRENT APPLICATION NUMBER: US/10/664,234
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2

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QY	181	CATGAAGTGAAATTAATGTGGAATGCTGTGCCACTTGCTCTGGGTAGCCAATGA	240
DB	181	CATGAAGTGAAATTAATGTGGAATGCTGTGCCACTTGCTCTGGGTAGCCAATGA	240
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DB	361	CCTCAAGTGGCTGAATGCGCAGCAGGTGCAAGCACTGCCCATGTGTGCCAGAGTGT	420
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DB	421	GAAATTCAAGAGTGAAGCCCGTCCGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	480
QY	481	AGCCCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	540
DB	481	AGCCCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC	540
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QY	661	ATAAGTAAACTCATTAAGTTCAGATTCGATCCTGGTGCAGCTGCAGGATGCAAGC	720
DB	661	ATAAGTAAACTCATTAAGTTCAGATTCGATCCTGGTGCAGCTGCAGGATGCAAGC	720
QY	721	TTAGTATTTCTATAGTGTACCTAAATAGCTTGGCTAATCATGTGATGCTTTTCT	780
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QY	781	GTGTGAATTTGTTATTCGCTCAATTCACATATGAGCCGGAAGCATAAAGTGT	840
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	2637.2	77.5	8854	3	US-09-053-549-1 Sequence 1, Appli
7	2634.6	77.4	4201	3	US-09-792-568-7 Sequence 7, Appli
8	2628.6	77.2	5767	3	US-09-810-861B-3 Sequence 3, Appli
9	2627.6	77.2	3796	3	US-09-470-661A-32 Sequence 32, Appli
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C 102	2410	70.8	19307	3	US-08-836-022A-10	Sequence 10, Appl
C 103	2410	70.8	19307	3	US-09-427-048A-10	Sequence 10, Appl
C 104	2408.4	70.8	6515	3	US-09-569-975-13	Sequence 13, Appl
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C 106	2401.6	70.6	4054	3	US-09-445-649-9	Sequence 9, Appl1
C 107	2400	70.5	4696	2	US-08-929-967-15	Sequence 15, Appl
C 108	2400	70.5	5158	2	US-08-929-967-16	Sequence 16, Appl
C 109	2400	70.5	7607	2	US-08-222-616-19	Sequence 19, Appl
C 110	2400	70.5	7607	3	US-08-446-648-19	Sequence 19, Appl
C 111	2400	70.5	7607	3	US-09-982-610-19	Sequence 19, Appl
C 112	2400	70.5	7607	6	PCT-US95-04228-19	Sequence 19, Appl
C 113	2400	70.5	9108	3	US-08-446-648-45	Sequence 45, Appl
C 114	2400	70.5	9108	3	US-09-982-610-45	Sequence 45, Appl
C 115	2400	70.5	9108	6	PCT-US95-04228-45	Sequence 45, Appl
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C 117	2391.6	70.3	3190	3	US-09-027-169-6	Sequence 6, Appl1
C 118	2391.6	70.3	3383	3	US-09-891-865B-3	Sequence 3, Appl1
C 119	2391.6	70.3	3444	3	US-09-891-865B-1	Sequence 1, Appl1
C 120	2391.6	70.3	3819	3	US-09-042-353-393	Sequence 393, App
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C 122	2391.6	70.3	3881	3	US-09-042-353-369	Sequence 369, App
C 123	2391.6	70.3	3881	3	US-08-758-417A-217	Sequence 217, App
C 124	2391.6	70.3	4189	3	US-09-891-865B-5	Sequence 5, Appl1
C 125	2391.6	70.3	4278	3	US-09-503-799-2	Sequence 2, Appl1
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C 129	2391.6	70.3	5822	3	US-09-891-865B-8	Sequence 8, Appl1
C 130	2391.6	70.3	6269	3	US-09-891-865B-9	Sequence 9, Appl1
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C 138	2390.6	70.2	5679	3	US-08-812-829-9	Sequence 9, Appl1
C 139	2390.6	70.2	5697	3	US-08-814-052-11	Sequence 11, Appl
C 140	2390.6	70.2	5697	3	US-08-812-829-11	Sequence 11, Appl
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C 142	2390.2	70.2	5181	3	US-09-498-599-5	Sequence 5, Appl1
C 143	2390	70.2	3343	9	5453363-2	Patent No. 5453363
C 144	2328.8	68.4	4454	2	US-07-712-284-1	Sequence 1, Appl1
C 145	2328.8	68.4	4454	6	PCT-US92-04227-1	Sequence 1, Appl1
C 146	2328.8	68.4	4732	2	US-07-884-811-1	Sequence 1, Appl1
C 147	2328.8	68.4	4732	2	US-07-885-971-1	Sequence 1, Appl1
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C 150	2328.8	68.4	4732	2	US-08-194-087-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-343-401A-3
; Sequence 3, Application US/08343401A
; Patent No. 5661132
; GENERAL INFORMATION:
; APPLICANT: Swain, William F
; APPLICANT: Macklin, Michael D
; APPLICANT: Ericksen, Elof
; APPLICANT: Andree, Christophe
; TITLE OF INVENTION: Improved Wound Healing
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: PO Box 2113
; CITY: Madison

;	STATE: WI	
;	COUNTRY: USA	
;	ZIP: 53701-2113	
;	COMPUTER READABLE FORM:	
;	MEDIUM TYPE: Floppy disk	
;	COMPUTER: IBM PC compatible	
;	OPERATING SYSTEM: PC-DOS/MS-DOS	
;	SOFTWARE: PatentIn Release #1.0, Version #1.30	
;	CURRENT APPLICATION DATA:	
;	APPLICATION NUMBER: US/08/343,401A	
;	FILING DATE: 22-NOV-1994	
;	CLASSIFICATION: 514	
;	ATTORNEY/AGENT INFORMATION:	
;	NAME: Seay, Nicholas J	
;	REGISTRATION NUMBER: 27,386	
;	REFERENCE/DOCKET NUMBER: 11-229-9103-9	
;	TELECOMMUNICATION INFORMATION:	
;	TELEPHONE: 608-251-5000	
;	TELEFAX: 608-251-9166	
;	INFORMATION FOR SEQ ID NO: 3:	
;	SEQUENCE CHARACTERISTICS:	
;	LENGTH: 4283 base pairs	
;	TYPE: nucleic acid	
;	STRANDEDNESS: double	
;	TOPOLOGY: circular	
;	MOLECULE TYPE: DNA (genomic)	
;	IMMEDIATE SOURCE:	
;	CLONE: pWRG1630	
;	FEATURE:	
;	NAME/KEY: exon	
;	LOCATION: 713..721	
;	FEATURE:	
;	NAME/KEY: exon	
;	LOCATION: 981..1253	
;	FEATURE:	
;	NAME/KEY: CDS	
;	LOCATION: join(713..721, 981..1253)	
;	FEATURE:	
;	NAME/KEY: sig_peptide	
;	LOCATION: 713..1049	
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QY	891 CTCACGTCCCGCTTCCAGTCGGGAAACCTGTCGTCAGCTGCATTATGATCGGCCA	950
Db	1770 CTCACGTCCCGCTTCCAGTCGGGAAACCTGTCGTCAGCTGCATTATGATCGGCCA	1829
QY	951 ACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTCCGCTTCCTGCTCACTGACTC	1010
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QY	1011 GCTGCGCTCGTGTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGCGGTAATACG	1070
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OM nucleic - nucleic search, using sw model

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(without alignments)
12389.205 Million cell updates/sec

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Perfect score: 3404
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
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1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss8: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1001.6	29.4	1176	8	CX943193
5	984.8	28.9	1013	3	BM438846
6	950	27.9	1067	1	AU081137
7	949.8	27.9	1265	10	AG435223
8	944.4	27.7	1027	10	CL021190
9	923.2	27.1	951	8	CV983341
10	919.2	27.0	1004	1	AJ281480
11	918.6	27.0	1089	1	AU081124
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18	885.6	26.0	893	11	DE101806
19	885	26.0	928	7	CO487414
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51	856.6	25.2	866	11	DE104168	DE104168 Oryzias 1
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c	130	816	24.0	1025	10	CL021193	CL021193 CH216-8A1
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c	149	806.6	23.7	816	11	DE099569	DE099569 Oryzias 1
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ALIGNMENTS

RESULT 1
AJ281552 1070 bp mRNA linear EST 30-JUN-2000
LOCUS AJ281552
DEFINITION 4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
ACCESSION AJ281552
VERSION AJ281552.1 GI:6929432
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.

REFERENCE 1 (bases 1 to 1070)
AUTHORS Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C., Donohue,M., Schultz,J., Benes,V., Bork,P., Anborg,W., Soares,M.B. and Kafatos,F.C.
TITLE Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
PUBMED 10841561
COMMENT Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
location/Qualifiers
1..1070
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/note="Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 30.9%; Score 1051; DB 1; Length 1070;
Best Local Similarity 99.4%; Pred. No. 4.9e-293;
Matches 1065; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1156 TTGCTGGCGTTTTCGATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGCTCA 1215
1 TTGCTGGCGTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGCTCA 60
QY 1216 AGTCAGAGGTGGCGAAACCCGACGAGCTATTAAGATACCAAGCGTTTCCCGTGAAGC 1275
61 AGTCAGAGGTGGCGAAACCCGACGAGCTATTAAGATACCAAGCGTTTCCCGTGAAGC 120
QY 1276 TCCCTGCGCTCTCTCTGTACCGACCTGCGGCTTACCGGATACCTGCGCCTTCTC 1335
121 TCCCTGCGCTCTCTCTGTACCGACCTGCGGCTTACCGGATACCTGCGCCTTCTC 180
QY 1336 CCTTCGGGAAGCGTGGCGCTTTCATAGCTCAAGCTGTAGGTATCTCAGTTCGGGTAG 1395
181 CCTTCGGGAAGCGTGGCGCTTTCATAGCTCAAGCTGTAGGTATCTCAGTTCGGGTAG 240
QY 1396 GTCGTTGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCC 1455
241 GTCGTTGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCC 300
QY 1456 TTATCCGTAATCTGTTGAGACCAACCCGTAAGACACGACTTATCGCACTGGCA 1515
301 TTATCCGTAATCTGTTGAGACCAACCCGTAAGACACGACTTATCGCACTGGCA 360
QY 1516 GCAGCCTGTGTACAGGATTAGCAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTG 1575
361 GCAGCCTGTGTGTACAGGATTAGCAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTG 420
QY 1576 AAGTGTGGCTTAACGAGGCTACACTAGGAAGACAGTATTGGTATCTGCGCTGTGCTG 1635
421 AAGTGTGGCTTAACGAGGCTACACTAGGAAGACAGTATTGGTATCTGCGCTGTGCTG 480
QY 1636 AAGCAGTTACCTTCGAAAAAGAGTTGTAGCTCTGTATCCGGCAAAACACCGGCT 1695
481 AAGCAGTTACCTTCGAAAAAGAGTTGTAGCTCTGTATCCGGCAAAACACCGGCT 540

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2006, 06:39:27 ; Search time 1926 Seconds
(without alignments)
11779.135 Million cell updates/sec

Title: US-10-664-234-18
Perfect score: 3404
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 segs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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12:	geneseqn2004as:*
13:	geneseqn2004bs:*
14:	geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2699.2	79.3	2743	14	ADZ78426	Adz78426 Alpha-fra
5	2690.8	79.0	4283	2	AAT86449	Aat86449 DNA encod
6	2690.8	79.0	4283	2	AAT86610	Aat86610 Epidermi
7	2690.8	79.0	4283	3	AAA63237	Aaa63237 Plasmid p
8	2690.8	79.0	4283	9	ABX93095	Abx93095 DNA seque
9	2690.8	79.0	4283	12	ADJ98301	Adj98301 Plasmid p
10	2677.2	78.6	8237	6	AAL45377	Aal45377 Recombina
11	2639.2	77.5	4082	6	AAD33877	Aad33877 PLM17 vec
12	2639.2	77.5	5143	13	ADT66834	Adt66834 MVA shutt
13	2639.2	77.5	7173	14	ADY99889	Ady99889 Exemplary
14	2639.2	77.5	8618	12	ADQ91623	Adq91623 Plasmid p
15	2637.2	77.5	8854	2	AAZ20086	Aaz20086 DNA encod
16	2636.4	77.5	5326	13	ADT66833	Adt66833 MVA shutt
17	2636.4	77.5	12225	6	AAD46400	Aad46400 PLW-48 pl
18	2636.4	77.5	12225	10	ADB06532	Adb06532 Plasmid t
19	2636.4	77.5	12225	13	ADT66779	Adt66779 Plasmid p

C	20	2634.6	77.4	4201	6	AB553597	Ab553597 Nourseoth
	21	2634	77.4	10600	11	ADM68432	Adm68432 Celery CE
	22	2634	77.4	10600	12	ADP26585	Adp26585 TMV CEL I
	23	2634	77.4	10600	13	ADQ88407	Adq88407 p1177MP4-
	24	2634	77.4	10600	13	ADSI17161	Adsi17161 p1177 MP4
	25	2634	77.4	10624	11	ADM68433	Adm68433 Celery CE
	26	2634	77.4	10624	12	ADP26586	Adp26586 TMV CEL I
	27	2634	77.4	10624	13	ADQ88408	Adq88408 p1177MP4-
	28	2634	77.4	10624	13	ADSI17162	Adsi17162 p1177 MP4
	29	2634	77.4	11222	12	ADN97500	Adn97500 Artificia
C	30	2633.6	77.4	3858	5	AAD04947	Aad04947 Plasmid p
C	31	2633.6	77.4	4886	6	ABT08169	Abt08169 Recombina
C	32	2633.6	77.4	4905	6	ABT08170	Abt08170 Recombina
C	33	2633.6	77.4	4960	4	AAD09269	Aad09269 pCMV-I-Cr
C	34	2633.6	77.4	4960	6	ABT08148	Abt08148 Recombina
C	35	2633.6	77.4	5290	6	ABT08171	Abt08171 Recombina
C	36	2633.6	77.4	5309	6	ABT08172	Abt08172 Recombina
C	37	2633.6	77.4	5430	12	ADN11355	Adn11355 GAGS-tet
C	38	2633.6	77.4	5711	6	ABT08145	Abt08145 Recombina
C	39	2633.6	77.4	5723	6	ABT08147	Abt08147 Recombina
C	40	2633.6	77.4	5730	6	ABT08168	Abt08168 Recombina
C	41	2633.6	77.4	5741	10	ADB81340	Adb81340 Codon opt
C	42	2633.6	77.4	5878	6	ABT08199	Abt08199 Recombina
C	43	2633.6	77.4	5878	12	ADN11357	Adn11357 CAGGS-cre
C	44	2633.6	77.4	6641	6	ABT08200	Abt08200 Recombina
C	45	2633.6	77.4	7332	4	AAD09270	Aad09270 pCMV-I-be
C	46	2633.6	77.4	7332	12	ADN11356	Adn11356 CMV-LacZ
	47	2632.6	77.3	4346	8	ABT16615	Abt16615 Artificia
	48	2632.6	77.3	4346	10	ACC44716	Acc44716 Plasmid p
	49	2632.6	77.3	5410	6	ABV74267	Abv74267 Plant spe
	50	2632.6	77.3	5410	6	ABQ76789	Abq76789 pUC19 pro
	51	2632.6	77.3	5410	12	ADH50772	Adh50772 Promoter-
	52	2632.6	77.3	5410	13	ADR49331	Adr49331 Plant exp
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C	54	2632.6	77.3	7208	8	ABZ81882	Abz81882 Plasmid p
	55	2632.6	77.3	8062	5	AAD04946	Aad04946 Plasmid p
	56	2632.6	77.3	8153	5	AAD04945	Aad04945 Plasmid p
	57	2632.6	77.3	8752	12	ADK51933	Adk51933 Novel rRN
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	60	2631	77.3	2803	12	ADI36474	Adi36474 Plasmid A
	61	2630.8	77.3	6565	5	AAF55126	Aaf55126 Nucleotid
	62	2630.8	77.3	6971	5	AAF55124	Aaf55124 Nucleotid
	63	2630.8	77.3	7558	5	AAF55125	Aaf55125 Nucleotid
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C	67	2630.4	77.3	6818	10	ACF58342	Acfs58342 Nucleotid
	68	2629.6	77.3	6069	13	ADR31624	Adr31624 Human CMV
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C	70	2628.8	77.2	6536	10	ADA44796	Ada44796 Microbial
C	71	2628.6	77.2	5767	6	AAS17547	Aas17547 Plasmid p
C	72	2628.6	77.2	6287	6	AAK98923	Aak98923 Human pMS
C	73	2628.6	77.2	6347	6	AAK98930	Aak98930 Human pMS
C	74	2628.6	77.2	9937	13	ADT04846	Adt04846 Vector DN
C	75	2628.6	77.2	15965	14	AE817031	Aeb17031 Targeting
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	77	2627.6	77.2	6295	2	AAV02043	Aav02043 Plasmid p
	78	2627.6	77.2	7164	5	AAD10238	Aad10238 Commercia
	79	2627.6	77.2	7383	5	AAS00153	Aas00153 Matrix me
C	80	2625.8	77.1	4045	2	AAQ70942	Aaq70942 Plasmid p
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C	83	2625.8	77.1	6898	2	AAV63742	Aav63742 Plasmid U
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	89	2623.4	77.1	9780	2	AAV82817	Aav82817 Plasmid p
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	92	2621.6	77.0	4016	8	AB555906	Ab555906 Lyme dise

93	2621.6	77.0	4950	2	AAV03801	AAV03801 Retrovira
94	2621.6	77.0	4950	4	AAC82936	AAC82936 Transdom1
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96	2621.6	77.0	4950	10	AAD60526	Aad60526 Retrovira
97	2621.6	77.0	4950	10	ADD28942	Add28942 Retrovira
98	2621.6	77.0	4950	14	ADY21075	Ady21075 Transdom1
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105	2621.6	77.0	6505	9	ADA12886	Ada12886 Murine MS
106	2621.6	77.0	6963	14	ADZ20362	Adz20362 Retrovira
107	2621.6	77.0	6983	14	AEB47895	Aeb47895 Vector pE
108	2621.6	77.0	8134	14	AEA02106	Aea02106 PRET1101R
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110	2621.6	77.0	8497	14	AEA02112	Aea02112 PRET1001R
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112	2621.6	77.0	9164	2	AAx82259	Aax82259 Beta-doma
113	2621.6	77.0	9431	12	AD007634	Ado07634 Expressio
114	2621.6	77.0	9632	2	AAx04251	Aax04251 Baculovir
115	2621.6	77.0	11158	14	ADY85094	Ady85094 ALVAC don
116	2621.6	77.0	11480	14	ADY85095	Ady85095 ALVAC don
117	2621.6	77.0	11846	2	AAx82261	Aax82261 Factor VI
118	2621.6	77.0	12022	2	AAx82260	Aax82260 Factor VI
119	2621.6	77.0	12200	14	ADV34803	Adv34803 Vector pA
120	2620.6	77.0	10130	6	AAD39129	Aad39129 p1044-Bol
121	2620.4	77.0	10607	10	ADF62076	Adf62076 Vector p1
122	2620.4	77.0	10631	10	ADF62077	Adf62077 Vector p1
123	2620.2	77.0	7566	2	AAQ42160	Aaq42160 Plasmid p
124	2620.2	77.0	7639	2	AAQ42159	Aaq42159 Plasmid p
125	2620	77.0	4163	2	AAQ32349	Aaq32349 Template
126	2618.4	76.9	4713	2	AAV12067	Aav12067 Murine 1A
127	2618.4	76.9	4724	2	AAV12068	Aav12068 Murine 1A
128	2618.4	76.9	5421	3	AAC68299	Aac68299 SV40/APPA
129	2618.4	76.9	5455	13	ADSI18609	Adsi18609 Expressio
130	2618.4	76.9	5465	2	AAZ20088	Aaz20088 Plasmid p
131	2618.4	76.9	5598	13	ADSI18611	Adsi18611 Expressio
132	2618.4	76.9	6116	3	AAC68297	Aac68297 R15/APPA
133	2618.4	76.9	6708	3	AAC68295	Aac68295 R15/APPA
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136	2617	76.9	6464	14	AEA04981	Aea04981 Retrovira
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138	2617	76.9	7244	14	AEA04979	Aea04979 Retrovira
139	2616.8	76.9	7560	4	AAC85599	Aac85599 Plasmid p
140	2616.8	76.9	7560	9	ADA09849	Ada09849 PiggyBac
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142	2615.6	76.8	7380	2	AAx84028	Aax84028 MMP9 prom
143	2614.2	76.8	6350	2	AAT35198	Aat35198 Plasmid p
144	2613.2	76.8	3796	3	AAA27831	Aaa27831 Vector p1
145	2612.8	76.8	8742	14	AEA43220	Aea43220 M. smegma
146	2612.4	76.7	7027	10	ACF58341	Acf58341 Nucleotid
147	2612	76.7	4949	10	ABX04119	Abx04119 Retrovira
148	2611.6	76.7	10065	14	AEB30772	Aeb30772 Modified
149	2611.4	76.7	9690	2	AAx76518	Aax76518 Plasmid p
150	2611.4	76.7	9690	9	ADB17614	Adb17614 Plasmid #

ALIGNMENTS

RESULT 1
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ID ADY71944 standard; DNA; 3404 BP.
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AC ADY71944;
XX
DT 02-JUN-2005 (first entry)
XX
DE Vector pGIS1.
XX

KW	cloning; mapping; ditag; vector; ss.
XX	
OS	Synthetic.
XX	
PN	US2005059022-A1.
XX	
PD	17-MAR-2005.
XX	
PF	17-SEP-2003; 2003US-00664234.
XX	
PR	17-SEP-2003; 2003US-00664234.
XX	
PA	(SCTE-) AGENCY SCI TECHNOLOGY & RES.
XX	
PI	Ruan Y, Ng P, Wei C;
XX	
DR	WPI; 2005-240897/25.
XX	
PT	New isolated oligonucleotides comprising at least one ditag, useful for
PT	gene identification signature analysis or for gene discovery or genome
PT	mapping.
PS	Claim 20; SEQ ID NO 18; 33pp; English.
XX	
CC	The invention relates to an isolated oligonucleotide comprising at least
CC	one ditag, where the ditag includes 2 joined first and second sequence
CC	tags, where the first tag includes a 5'-terminus sequence and the second
CC	tag comprises the 3'-terminus sequence of a nucleic acid molecule or its
CC	fragment. The oligonucleotide further comprises two adapter sequence
CC	(preferably containing restriction enzyme sites) flanking the ditags. The
CC	composition and methods using it are useful for gene identification
CC	signature analysis, for gene discovery or genome mapping or for isolating
CC	full length cDNAs. These may also be used for measuring transcript
CC	abundance in transcriptsomes, for annotating genome sequences or for
CC	enhancing sequencing efficiency. This sequence corresponds to the vector
CC	pgis1 containing a ditag oligonucleotide sequence of the invention.
XX	
SO	Sequence 3404 BP; 812 A; 872 C; 894 G; 826 T; 0 U; 0 Other;
	Query Match 100.0%; Score 3404; DB 14; Length 3404;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 3404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB	1 GGGCGAATTCCTCGAGCGCGCGGATCCGACGAGAGCGCCTGCTACGGCTCGCGCGGT 60
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QY	181 CATGAAGGTGAATAATTAATGTTGGAATGCTGGCCACTTGGCTCTGGGTAAGCCAATGA 240
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QY	241 TGAGAACTGCGGCATCTGCAGGATGGCGTTTAATGGCTGCTGTCCAGACTGTAAAGTGGC 300
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QY	301 TGGTGATGACTGCCCCCTCGTGTGGGACAGTGTCTCCCACTGCTTCCACATGCACTGCAT 360
DB	301 TGGTGATGACTGCCCCCTCGTGTGGGACAGTGTCTCCCACTGCTTCCACATGCACTGCAT 360
QY	361 CCTCAAGTGCGTGAATGCGCAGCAGGTGCGACGACACTGCCCATGTGTCCCAAGAGTGTG 420
DB	361 CCTCAAGTGCGTGAATGCGCAGCAGGTGCGACGACACTGCCCATGTGTGTCCCAAGAGTGTG 420
QY	421 GAAGTTCAAAGAGTGAAGCCCGTGCGGCTGCACTTCCCTCTCTGTGTGTCGACGGCTC 480
DB	421 GAAGTTCAAAGAGTGAAGCCCGTGCGGCTGCACTTCCCTCTCTGTGTGTCGACGGCTC 480

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2006, 07:14:47 ; Search time 16857 Seconds
(without alignments)
11478.621 Million cell updates/sec

Title: US-10-664-234-18
Perfect score: 3404
Sequence: 1 ggsgcaattctcgagcgcc.....ttgtaatacgaactactata 3404

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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2: gb_in:*
3: gb_env:*
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9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2699.2	79.3	2743	11 CVPGE3Z	X65304 Cloning vec
3	2690.8	79.0	4283	6 I63120	I63120 Sequence 3
4	2690.8	79.0	4283	6 I85496	I85496 Sequence 1
5	2679.8	78.7	10163	11 AY860671	AY860671 Expressio
6	2671.8	78.5	7528	11 AY608405	AY608405 Cysteine-
7	2650.6	77.9	4674	11 XXU02437	U02437 Cloning vec
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9	2649.2	77.8	3394	11 AF083407	AF083407 Cloning v
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11	2649.2	77.8	3617	11 AF083408	AF083408 Cloning v
12	2649.2	77.8	3714	11 AF083408	AF083408 Cloning v
13	2649.2	77.8	3946	11 AF134573	AF134573 Cloning v
14	2649.2	77.8	4026	11 AF062080	AF062080 Cloning v
15	2649.2	77.8	4154	11 AF062082	AF062082 Cloning v
16	2649.2	77.8	4503	11 AF062081	AF062081 Cloning v
17	2649.2	77.8	4795	11 AF134572	AF134572 Cloning v
18	2649.2	77.8	4795	11 AF134572	AF134572 Cloning v

19	2649.2	77.8	5263	11 AY652436	AY652436 Promoter-
20	2649.2	77.8	5486	11 AY652435	AY652435 Promoter-
21	2649.2	77.8	5895	11 AY652434	AY652434 Promoter-
22	2649.2	77.8	6023	11 AY652437	AY652437 Promoter-
23	2649.2	77.8	6664	11 AY652438	AY652438 Promoter-
24	2647.8	77.8	2746	11 CVPGE4Z	X65305 Cloning vec
25	2639.2	77.5	4082	6 AX451393	AX451393 Sequence
26	2639.2	77.5	5143	6 CQ891775	CQ891775 Sequence
27	2639.2	77.5	7387	6 AR176236	AR176236 Sequence
28	2639.2	77.5	7387	6 BD195025	BD195025 Equine in
29	2639.2	77.5	7387	6 AX003207	AX003207 Chimeric
30	2637.2	77.5	8854	6 BD194452	BD194452 Sequence
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32	2636.4	77.5	12225	6 CQ891719	CQ891719 Sequence
33	2634.6	77.4	4201	6 AR477983	AR477983 Sequence
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35	2633.6	77.4	3858	6 AX114873	AX114873 Sequence
36	2633.6	77.4	4960	6 AX191663	AX191663 Sequence
37	2633.6	77.4	5430	6 CQ803130	CQ803130 Sequence
38	2633.6	77.4	5711	6 AX114861	AX114861 Sequence
39	2633.6	77.4	5741	6 AX816381	AX816381 Sequence
40	2633.6	77.4	5878	6 CQ803132	CQ803132 Sequence
41	2633.6	77.4	7332	6 CQ803131	CQ803131 Sequence
42	2633.6	77.4	7332	6 AX191664	AX191664 Sequence
43	2633.4	77.4	4252	11 D0077692	D0077692 Cloning v
44	2633.4	77.4	4473	11 UCT89964	U89964 Cloning vec
45	2632.6	77.3	5410	6 CQ874871	CQ874871 Sequence
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47	2632.6	77.3	5410	6 AX481627	AX481627 Sequence
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49	2632.6	77.3	5410	6 AX951597	AX951597 Sequence
50	2632.6	77.3	5410	6 AX961452	AX961452 Sequence
51	2632.6	77.3	7208	6 AX712171	AX712171 Sequence
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53	2632.6	77.3	8153	6 AX114871	AX114871 Sequence
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57	2630	77.3	3536	11 AY157312	AY157312 Cloning v
58	2630	77.3	3818	11 AY157311	AY157311 Cloning v
59	2630	77.3	3868	11 AY157308	AY157308 Cloning v
60	2630	77.3	4314	11 AY157310	AY157310 Cloning v
61	2630	77.3	7877	11 AY157309	AY157309 Cloning v
62	2629.4	77.2	5647	1 BACXNB	D29979 Bacillus st
63	2629.4	77.2	11612	11 CUV80929	U80929 Cloning vec
64	2629.4	77.2	13397	11 AY487253	AY487253 Cloning v
65	2629.4	77.2	13462	11 AY487252	AY487252 Cloning v
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67	2629.4	77.2	16437	11 AF123770	AF123770 Shuttle v
68	2629.4	77.2	18772	11 AF133437	AF133437 Cloning v
69	2629.4	77.2	19500	11 CUV75992	UV75992 Cloning vec
70	2629.4	77.2	22960	11 AY192024	AY192024 BAC cloni
71	2628.6	77.2	5767	6 AR575401	AR575401 Sequence
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73	2628.6	77.2	15965	6 CQ894659	CQ894659 Sequence
74	2627.6	77.2	3734	11 AY122059	AY122059 Expressio
75	2627.6	77.2	3734	11 AY122060	AY122060 Expressio
76	2627.6	77.2	3796	6 B49323	E49323 Infectious
77	2627.6	77.2	3796	6 AR269181	AR269181 Sequence
78	2627.6	77.2	3796	6 BD015906	BD015906 Infectiou
79	2627.6	77.2	3796	6 BD016274	BD016274 Infectiou
80	2627.6	77.2	4518	11 XXP35SGFP	U28417 Cloning vec
81	2627.6	77.2	4519	11 U02456	U02456 Cloning vec
82	2627.6	77.2	5667	11 AF502128	AF502128 Transient
83	2627.6	77.2	6541	11 XXU02433	U02433 Cloning vec
84	2627.6	77.2	6894	11 XXU02435	U02435 Cloning vec
85	2627.6	77.2	7069	11 U02442	U02442 Cloning vec
86	2627.6	77.2	7164	6 AX195206	AX195206 Sequence
87	2627.6	77.2	7164	11 U02451	U02451 Cloning vec
88	2627.6	77.2	7383	6 AR474280	AR474280 Sequence
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C 92	2626.6	77.2	23250	11	AY336796	AY336796 Transform
C 93	2626.4	77.2	5027	11	AF276982	AF276982 Integrat1
C 94	2626.2	77.2	4324	11	AY894753	AY894753 Reporter
C 95	2625.8	77.1	4045	6	AR152249	AR152249 Sequence
C 96	2625.8	77.1	5848	6	BD263361	BD263361 Compositi
C 97	2625.8	77.1	5897	6	BD132716	BD132716 Regulator
C 98	2625.8	77.1	5897	6	AR209019	AR209019 Sequence
C 99	2625.8	77.1	5897	6	AR482088	AR482088 Sequence
C 100	2625.8	77.1	6898	6	BD132717	BD132717 Regulator
C 101	2625.8	77.1	6898	6	AR209020	AR209020 Sequence
C 102	2625.8	77.1	6898	6	AR482089	AR482089 Sequence
C 103	2625.4	77.1	4776	6	A95117	A95117 Sequence 1
C 104	2625.4	77.1	4776	6	A95152	A95152 Sequence 1
C 105	2625.4	77.1	4776	6	AR304364	AR304364 Sequence
C 106	2625.4	77.1	9335	6	BD132709	BD132709 Regulator
C 107	2625.4	77.1	9335	6	AR209012	AR209012 Sequence
C 108	2625.4	77.1	9335	6	AR482081	AR482081 Sequence
C 109	2623.6	77.1	5452	11	U02454	U02454 Cloning vec
C 110	2623.4	77.1	9639	6	AR287383	AR287383 Sequence
C 111	2623.4	77.1	9780	6	AR82653	AR82653 Sequence 3
C 112	2623.4	77.1	9780	6	BD107672	BD107672 Pharmaceu
C 113	2623.4	77.1	10511	6	AX666316	AX666316 Sequence
C 114	2623.4	77.1	10517	6	AX666208	AX666208 Sequence
C 115	2623.4	77.1	11099	6	E16636	E16636 Expression
C 116	2623.4	77.1	11099	6	E16677	E16677 A11 sequenc
C 117	2621.6	77.0	4016	6	AR231273	AR231273 Sequence
C 118	2621.6	77.0	4311	6	AX244155	AX244155 Sequence
C 119	2621.6	77.0	4950	6	AR119454	AR119454 Sequence
C 120	2621.6	77.0	4950	6	AR202762	AR202762 Sequence
C 121	2621.6	77.0	4950	6	AR231742	AR231742 Sequence
C 122	2621.6	77.0	4950	6	AR535385	AR535385 Sequence
C 123	2621.6	77.0	4950	6	AR616632	AR616632 Sequence
C 124	2621.6	77.0	5733	6	BD271904	BD271904 Process f
C 125	2621.6	77.0	5733	15	ANGPDAG	Z32524 A.nidulans
C 126	2621.6	77.0	5760	11	EVSPAN24	Z32750 Expression
C 127	2621.6	77.0	6143	6	AX823826	AX823826 Sequence
C 128	2621.6	77.0	6505	6	AX823827	AX823827 Sequence
C 129	2621.6	77.0	6779	11	AJ810977	AJ810977 Cloning v
C 130	2621.6	77.0	6963	6	CS103184	CS103184 Sequence
C 131	2621.6	77.0	8887	11	AB084895	AB084895 Expressio
C 132	2621.6	77.0	9164	6	BD234664	BD234664 Novel vec
C 133	2621.6	77.0	9164	6	AR428618	AR428618 Sequence
C 134	2621.6	77.0	9431	11	AY491501	AY491501 Expressio
C 135	2621.6	77.0	9599	15	AY337720	AY337720 Trichoder
C 136	2621.6	77.0	9632	6	BD085143	BD085143 Ricin-lik
C 137	2621.6	77.0	9632	6	AR359204	AR359204 Sequence
C 138	2621.6	77.0	9632	6	AR590299	AR590299 Sequence
C 139	2621.6	77.0	11846	6	BD234666	BD234666 Novel vec
C 140	2621.6	77.0	11846	6	AR428620	AR428620 Sequence
C 141	2621.6	77.0	12022	6	BD234665	BD234665 Novel vec
C 142	2621.6	77.0	12022	6	AR428619	AR428619 Sequence
C 143	2621.6	77.0	12494	15	D84238	D84238 Nicotiana t
C 144	2621.6	77.0	15528	6	A93016	A93016 Sequence 4
C 145	2621.6	77.0	15528	11	PEAVGEN	Y07862 Cloning vec
C 146	2620.6	77.0	5670	11	EVSPAN522	Z32688 Expression
C 147	2620.6	77.0	5670	11	EVSPAN523	Z32689 Expression

ALIGNMENTS

RESULT 1			
CS091374	CS091374	3404 bp	DNA linear PAT 03-JUN-2005
LOCUS	Sequence 18 from Patent EP1533386.		
DEFINITION	CS091374		
ACCESSION	CS091374		
VERSION	CS091374.1		GI:66948703
KEYWORDS	.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Ruan,Y., Ng,P. and Wei,C.	Method for gene identification signature (GIS) analysis	Patent: EP 153386-A 18 25-MAY-2005;
		Agency for Science, Technology and Research (SG)	Location/Qualifiers
FEATURES	source	1..3404	/organism="synthetic construct"
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			/db_xref="taxon:32630"
			/note="sequence of pGIS1"
		15..704	/note="region from 15 to 704 represents the stuffer fragment, comprising MmeI and BamHI, that is removed during cloning"
ORIGIN			
Query Match	100.0%;	Score 3404;	DB 6; Length 3404;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 3404;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
QY	1	GGGCGAATTCCTGAGCGCGCCGGATCCGACGAGAGCGCTGCGTACGGCTCGCCGGGT	60
Dd	1	GCGCGAATTCCTGAGCGCGCCGGATCCGACGAGAGCGCTGCGTACGGCTCGCCGGGT	60
QY	61	GGCTGGCGCTACTTCGAGAGACCAGCGCGCGCGGTCTTTTATACATTCCCGCGG	120
Dd	61	GGCTGGCGCTACTTCGAGAGACCAGCGCGCGCGGTCTTTTATACATTCCCGCGG	120
QY	121	GAGCAACGGAAGGCGCGGCCCTCGTGATTAGCGCGCGAGGTACAAGGCTCTGTGT	180
Dd	121	GAGCAACGGAAGGCGCGGCCCTCGTGATTAGCGCGCGAGGTACAAGGCTCTGTGT	180
QY	181	CATGAAGGTGAATAATTAAATGTGGAATGTTGGCATGTTGGCCTTGGGTAGCCAATGA	240
Dd	181	CATGAAGGTGAATAATTAAATGTGGAATGTTGGCATGTTGGCCTTGGGTAGCCAATGA	240
QY	241	TGAGAAGTGCAGCATCTGCAGAGATGGCGTTAATGGCTGCTGTCCAGACTGTAAAGTGGC	300
Dd	241	TGAGAAGTGCAGCATCTGCAGAGATGGCGTTAATGGCTGCTGTCCAGACTGTAAAGTGGC	300
QY	301	TGGTGATGACTGCCCCCTCGTGTGGGACAGTGTCTCCCACTGCTTCCACATGCACTGCAT	360
Dd	301	TGGTGATGACTGCCCCCTCGTGTGGGACAGTGTCTCCCACTGCTTCCACATGCACTGCAT	360
QY	361	CCTCAAGTGGCTGAATGCGCAGCAGGTGACAGCACACTGCCCAATGTGTGCCAGGAGTG	420
Dd	361	CCTCAAGTGGCTGAATGCGCAGCAGGTGACAGCACACTGCCCAATGTGTGCCAGGAGTG	420
QY	421	GAAATTCAAAGAGTGAAGCCCCTGCGCTGCCACTTCCCTCTCCTGTGCTGTGCCAGGCTC	480
Dd	421	GAAATTCAAAGAGTGAAGCCCCTGCGCTGCCACTTCCCTCTCCTGTGCTGTGCCAGGCTC	480
QY	481	AGCCCCCTTCCCTCCCTCCCTCCCTCCAGATACAGCACCCCAAGTCCCTCCACACAGCAC	540
Dd	481	AGCCCCCTTCCCTCCCTCCCTCCCTCCAGATACAGCACCCCAAGTCCCTCCACACAGCAC	540
QY	541	AGTGTGCCAGAGATCTCGGTCTGTGCCGGGACAAAGATGCTTCTGTGGCTGGGA	600
Dd	541	AGTGTGCCAGAGATCTCGGTCTGTGCCGGGACAAAGATGCTTCTGTGGCTGGGA	600
QY	601	CAAGGTGAAAAGAGCTTTGCTGACGTGTTTTTTCCATCACATGACACTTATTCA	660
Dd	601	CAAGGTGAAAAGAGCTTTGCTGACGTGTTTTTTCCATCACATGACACTTATTCA	660
QY	661	ATAAGTAATACTCATTAAGTTCGAAGTCGATCCTGGTGCACTGACGGCATGCAAGC	720
Dd	661	ATAAGTAATACTCATTAAGTTCGAAGTCGATCCTGGTGCACTGACGGCATGCAAGC	720
QY	721	TTGAGTAATTCTAATGTCACCTTAATAAGCTTGGCGTAATCATGCTATAGCTGTTTCT	780
Dd	721	TTGAGTAATTCTAATGTCACCTTAATAAGCTTGGCGTAATCATGCTATAGCTGTTTCT	780